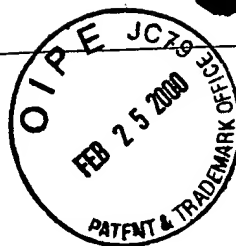


SEQUENCE LISTING



<110> Covacci, Antonello
Bugnoli, Massimo
Telford, John
Macchia, Giovanni
Rappuoli, Rino

<120> Helicobacter Pylori CAI Antigen Proteins Useful For
Vaccines And Diagnostics

<130> CHIR0157

<140> 09/360,685

<141> 1999-07-26

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 1

gcaagcttat cgatgtcgac tcgagct

27

<210> 2

<211> 3960

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 2

aaaaagaaag gaagaaaatg gaaatacaac aaacacaccg caaaatcaat cgccctctgg 60
tttctctcgc tttagttagga gcattagtca gcatcacacc gcaacaaagt catgccgcct 120
ttttcacaac cgtgatcatt ccagccattg ttgggggtat cgctacaggc accgctgtag 180
gaacgggtctc agggcttctt agctgggggc tcaaacaagc cgaagaagcc aataaaaccc 240
cagataaacc cgataaagtt tggcgcattc aagcaggaaa aggctttaat gaattccta 300

acaaggaata	cgacttatac	agatcccttt	tatccagtaa	gattgatgga	ggttgggatt	360
gggggaatgc	cgctaggcat	tattgggtca	aaggcgggca	acagaataag	cttgaagtgg	420
atatgaaaga	cgctgtaggg	acttatacct	tatcagggct	tagaaacttt	actggtgggg	480
athtagatgt	caatatgcaa	aaagccactt	tacgcttggg	ccaattcaat	ggcaattctt	540
ttacaagcta	taaggatagt	gctgatcgca	ccacgagagt	ggatttcaac	gctaaaaata	600
tctcaattga	taattttgta	gaaatcaaca	atcgtgtggg	ttctggagcc	gggaggaaag	660
ccagctctac	ggttttgact	ttgcaagctt	cagaagggat	cactagcgat	aaaaacgctg	720
aaattttctt	ttatgatggg	gccacgctca	atltggcttc	aagcagcggt	aaattaatgg	780
gtaatgtgtg	gatggggcgt	ttgcaatacg	tgggagcgta	tttggccctt	tcatacagca	840
cgataaacac	ttcaaaagta	acaggggaag	tgaattttta	ccacctcact	gttggcgata	900
aaaacgccgc	tcaagcgggc	attatcgcta	ataaaaagac	taatattggc	acactggatt	960
tgtggcgaag	cgccgggtta	aacattatcg	ctcctccaga	aggtggctat	aaggataaac	1020
ccaataatac	cccttctcaa	agtgggtgta	aaaacgacaa	aaatgaaagc	gctaaaaacg	1080
acaacaaga	gagcagtcac	aataatagta	acactcaggt	cattaaccca	cccaatagtg	1140
cgcaaaaaac	agaagttcaa	cccacgcaag	tcattgatgg	gccttttgcg	ggcggcaaac	1200
acacggttgt	caatatcaac	cgcatcaaca	ctaacgctga	tggcacgatt	agagtgggag	1260
ggttttaaagc	ttctcttacc	accaatgcgg	ctcatttgca	tatcggcaaa	ggcgggtgtca	1320
atctgtccaa	tcaagcgagc	gggcgctctc	ttatagtggg	aaatctaact	gggaatatca	1380
ccgttgatgg	gcctttaaga	gtgaataatc	aagtgggtgg	ctatgctttg	gcaggatcaa	1440
gcgcgaaatt	tgagtttaag	gctgggtacg	ataccaaaaa	cggcacagcc	acttttaata	1500
acgatattag	tctgggaaga	tttgtgaatt	taaaggtgga	tgctcataca	gctaatttta	1560
aaggtattga	tacgggtaat	ggtgggtttc	acaccttaga	ttttagtggc	gttacagaca	1620
aagtcaatat	caacaagctc	attacggctt	ccactaatgt	ggccgttaaa	aacttcaaca	1680
ttaatgaatt	gattgtttaa	accaatggga	taagtgtggg	ggaatatact	catttttagcg	1740
aagatatagg	cagtcaatcg	cgcatcaata	ccgtgcgttt	ggaaactggc	actaggtcac	1800
ttttctctgg	gggtgtttaa	tttaaagggt	gcgaaaaatt	ggttatagat	gagttttact	1860
atagcccttg	gaattatttt	gacgctagaa	atattaaaaa	tggtgaaatc	accaataaac	1920
ttgcttttgg	acctcaagga	agtccttggg	gcacatcaaa	acttatgttc	aataatctaa	1980
ccctagggtca	aaatgcggtc	atggattata	gccaattttc	aaattttaacc	attcaagggg	2040
atttcatcaa	caatcaaggc	actatcaact	atctggtccg	aggtgggaaa	gtggcaacct	2100
taagcgtagg	caatgcagca	gctatgatgt	ttaataatga	tatagacagc	gcgaccggat	2160
tttacaacc	gctcatcaag	attaacagcg	ctcaagatct	cattaaaaat	acagaacatg	2220
ttttattgaa	agcgaaaatc	attgggttat	gtaatgtttc	tacaggtacc	aatggcatta	2280
gtaatgttaa	tctagaagag	caattcaaac	agcgcctagc	cctttataac	aacaataacc	2340
gcatggatac	ttgtgtggtg	cgaaatactg	atgacattaa	agcatgcggg	atggctatcg	2400
gcgatcaaag	catggtgaac	aacctgaca	attacaagta	tcttatcggt	aaggcatgga	2460
aaaatatagg	gatcagcaaa	acagctaatt	gctctaaaa	ttcgggtgat	tatttaggca	2520
attctacgcc	tactgagaat	ggtggcaata	ccacaaaatt	accacaaaac	accactagca	2580
atgcacgttc	tgccaacaac	gcccttgca	aaaacgctcc	tttcgctcaa	cctagtgtca	2640
ctcctaattt	agtcgctatc	aatcagcatg	atlttggcac	tattgaaagc	gtgtttgaat	2700
tggctaaccg	ctctaaagat	attgacacgc	tttatgtctaa	ctcaggcgct	caaggcaggg	2760
atctcttaca	aaccttattg	attgatagcc	atgatgcggg	ttatgccaga	aaaatgattg	2820
atgctacaag	cgctaataag	atcaccaagc	aattgaatac	ggccactacc	acttttaaca	2880
acatagccag	tttagagcat	aaaaccagcg	gcttacaac	tttgagcttg	agtaatgcga	2940
tgatttttaa	ttctcgttta	gtcaatctct	ccaggagaca	caccaacat	attgactcgt	3000
tcgccaaaac	cttacaagct	ttaaaagacc	aaaaattcgc	ttcttttagaa	agcgcggcag	3060
aagtgttgta	tcaatttgcc	cctaaatatg	aaaaacctac	caatgtttgg	gctaacgcta	3120
ttgggggaac	gagcttgaat	aatgggtctc	acgcttcatt	gtatggcaca	agcgcggggc	3180

tagacgctta ccttaacggg caagtggaag ccattgtggg cggttttgga agctatggtt 3240
 atagctcttt taataatcgt gcgaactccc ttaactctgg ggccaataac actaattttg 3300
 gcgtgtatag ccgtattttt gcccaaccagc atgaatttga ctttgaagct caagggggcac 3360
 tagggagcga tcaatcaagc ttgaatttca aaagcgctct attacaagat ttgaatcaaa 3420
 gctatcatta cttagcctat agcgctgcaa caagagcgag ctatggttat gacttcgcgt 3480
 tttttaggaa cgcttttagtg ttaaaaccaa gcgtgggtgt gagctataac catttaggtt 3540
 caaccaactt taaaagcaac agcaccaatc aagtggcttt gaaaaatggc tctagcagtc 3600
 agcatttatt caacgctagc gctaattgtg aagcgcgcta ttattatggg gacatttcac 3660
 acttctacat gaatgctgga gttttacaag agttcgctca tgttggctct aataacgcgc 3720
 cgtctttaaa cacctttaaa gtgaatgccg ctgcgaaccc tttaaatacc catgccagag 3780
 tgatgatggg tggggaatta aaattagcta aagaagtgtt tttgaatttg ggcgttgttt 3840
 atttgcacaa tttgatttcc aatataggcc atttcgcttc caatttagga atgaggtata 3900
 gtttctaaat accgctctta aaccatgct caaagcatgg gtttgaaatc ttacaaaaca 3960

<210> 3

<211> 1296

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Sequence

<400> 3

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1 5 10 15

Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
 20 25 30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
 85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
 100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
 115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr
 130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
 145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
 165 170 175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
 180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
 195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
 210 215 220

Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp
 225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn
 245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
 260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
 275 280 285

His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala
 290 295 300

Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
 305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
 325 330 335

Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala
 340 345 350

Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val
 355 360 365

Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile
 385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe
 405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
 420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu
 435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
 450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
 465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
 485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
 500 505 510

Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
 515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
 530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
 545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
 565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr
 580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu
 595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg
 610 615 620

Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln
 625 630 635 640

Gly	Ser	Pro	Trp	Gly	Thr	Ser	Lys	Leu	Met	Phe	Asn	Asn	Leu	Thr	Leu	645	650	655
Gly	Gln	Asn	Ala	Val	Met	Asp	Tyr	Ser	Gln	Phe	Ser	Asn	Leu	Thr	Ile	660	665	670
Gln	Gly	Asp	Phe	Ile	Asn	Asn	Gln	Gly	Thr	Ile	Asn	Tyr	Leu	Val	Arg	675	680	685
Gly	Gly	Lys	Val	Ala	Thr	Leu	Ser	Val	Gly	Asn	Ala	Ala	Ala	Met	Met	690	695	700
Phe	Asn	Asn	Asp	Ile	Asp	Ser	Ala	Thr	Gly	Phe	Tyr	Lys	Pro	Leu	Ile	705	710	715
Lys	Ile	Asn	Ser	Ala	Gln	Asp	Leu	Ile	Lys	Asn	Thr	Glu	His	Val	Leu	725	730	735
Leu	Lys	Ala	Lys	Ile	Ile	Gly	Tyr	Gly	Asn	Val	Ser	Thr	Gly	Thr	Asn	740	745	750
Gly	Ile	Ser	Asn	Val	Asn	Leu	Glu	Glu	Gln	Phe	Lys	Glu	Arg	Leu	Ala	755	760	765
Leu	Tyr	Asn	Asn	Asn	Asn	Arg	Met	Asp	Thr	Cys	Val	Val	Arg	Asn	Thr	770	775	780
Asp	Asp	Ile	Lys	Ala	Cys	Gly	Met	Ala	Ile	Gly	Asp	Gln	Ser	Met	Val	785	790	795
Asn	Asn	Pro	Asp	Asn	Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	805	810	815
Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	820	825	830
Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu	835	840	845
Pro	Thr	Asn	Thr	Thr	Ser	Asn	Ala	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	850	855	860
Gln	Asn	Ala	Pro	Phe	Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	865	870	875
Ile	Asn	Gln	His	Asp	Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	885	890	895

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln		
900	905	910
Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly		
915	920	925
Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys		
930	935	940
Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu		
945	950	955 960
His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile		
965	970	975
Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile		
980	985	990
Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala		
995	1000	1005
Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr		
1010	1015	1020
Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu		
1025	1030	1035 1040
Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp		
1045	1050	1055
Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly Gly Phe Gly Ser		
1060	1065	1070
Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn Ser Leu Asn Ser Gly		
1075	1080	1085
Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln		
1090	1095	1100
His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser		
1105	1110	1115 1120
Ser Leu Asn Phe Lys Ser Ala Leu Leu Gln Asp Leu Asn Gln Ser Tyr		
1125	1130	1135
His Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp		
1140	1145	1150

Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val
 1155 1160 1165

Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn
 1170 1175 1180

Gln Val Ala Leu Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala
 1185 1190 1195 1200

Ser Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe
 1205 1210 1215

Tyr Met Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn
 1220 1225 1230

Asn Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro
 1235 1240 1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu Ala
 1250 1255 1260

Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile
 1265 1270 1275 1280

Ser Asn Ile Gly His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
 1285 1290 1295

<210> 4
 <211> 5925
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial
 Sequence

<400> 4
 ctccatttta agcaactcca tagaccacta aagaaacttt ttttgaggct atctttgaaa 60
 atctgtccta ttgatttggt ttccattttg tttcccatgt ggatcttggt gatcacaac 120
 gcttaattat acatgctata gtaagcatga cacacaaacc aaactatfff tagaacgctt 180
 catgtgtcca ccttgactaa ccattttotcc aaccatactt tagcggttgca tttgattttc 240
 tcaaaaagat tcattttctta tttcttggtc ttattaaagt tctttcattt tagcaaattt 300
 ttgttaattg tgggtaaaaa tgtgaatcgt cctagccttt agacgcctgc aacgatcggg 360

cttttttcaa	tattaataat	gattaatgaa	aaaaaaaaaa	aatgcttgat	attgttgtat	420
aatgagaatg	ttcaaagaca	tgaattgact	actcaagcgt	gtagcgattt	ttagcagtct	480
ttgacactaa	caagataccg	ataggtatga	aactaggtat	agtaaggaga	aacaatgact	540
aacgaaacca	ttgaccaaca	accacaaacc	gaagcggcct	ttaacccgca	gcaatttatc	600
aataatcttc	aagtagcttt	tcttaaagtt	gataacgctg	tcgcttcata	cgatcctgat	660
caaaaaccaa	tcgttgataa	gaacgatagg	gataacaggc	aagcttttga	aggaatctcg	720
caattaaggg	aagaatactc	caataaagcg	atcaaaaatc	ctaccaaaaa	gaatcagtat	780
ttttcagact	ttatcaataa	gagcaatgat	ttaatcaaca	aagacaatct	cattgatgta	840
gaatcttcca	caaagagctt	tcagaaattt	ggggatcagc	gttaccgaat	tttcacaagt	900
tgggtgtccc	atcaaaacga	tccgtctaaa	atcaacaccc	gatcgatccg	aaattttatg	960
gaaaatatca	tacaaccccc	tatccttgat	gataaagaga	aagcggagtt	tttgaaatct	1020
gccaaacaat	cttttgcagg	aatcattata	gggaatcaaa	tccgaacgga	tcaaaagttc	1080
atgggcgtgt	ttgatgagtc	cttgaaagaa	aggcaagaag	cagaaaaaaaa	tggagagcct	1140
actggtgggg	attggttgga	tatttttctc	tcattttatat	ttgacaaaaa	acaatcttct	1200
gatgtcaaag	aagcaatcaa	tcaagaacca	gttccccatg	tccaaccaga	tatagccact	1260
accaccaccg	acatacaagg	cttaccgcct	gaagctagag	atttacttga	tgaaaggggt	1320
aatttttcta	aattcactct	tggcgatatg	gaaatgttag	atgttgaggg	agtcgctgac	1380
attgatccca	attacaagtt	caatcaatta	ttgattcaca	ataacgctct	gtcttctgtg	1440
ttaatgggga	gtcataatgg	catagaacct	gaaaaagttt	cattgttgta	tgggggcaat	1500
ggtggtcctg	gagctaggca	tgattggaac	gccaccgttg	gttataaaga	ccaacaaggc	1560
aacaatgtgg	ctacaataat	taatgtgcat	atgaaaaacg	gcagtggtct	agtcatagca	1620
ggtggtgaga	aagggattaa	caaccctagt	ttttatctct	acaaagaaga	ccaactcaca	1680
ggctcacaac	gagcattaag	tcaagaagag	atccaaaaca	aaatagattt	catggaattt	1740
cttgcacaaa	ataatgctaa	attagacaac	ttgagcgaga	aagagaagga	aaaattccga	1800
actgagatta	aagattttcca	aaaagactct	aaggcttatt	tagacgcctt	agggaaatgat	1860
cgtatttgctt	ttgtttctaa	aaaagacaca	aaacattcag	ctttaattac	tgagtttggt	1920
aatggggatt	tgagctacac	tctcaaagat	tatgggaaaa	aagcagataa	agcttttagat	1980
agggagaaaa	atgttactct	tcaaggtagc	ctaaaacatg	atggcgtgat	gtttgttgat	2040
tatttctaatt	tcaaatacac	caacgcctcc	aagaatccca	ataagggtgt	aggcgttacg	2100
aatggcgttt	cccattttaga	agtaggcttt	aacaaggtag	ctatctttta	tttgcctgat	2160
ttaaataatc	tcgctatcac	tagtttcgta	aggcggaatt	tagaggataa	actaaccact	2220
aaaggattgt	ccccacaaga	agctaataag	cttatcaaag	attttttgag	cagcaacaaa	2280
gaattgggtg	gaaaaacttt	aaacttcaat	aaagctgtag	ctgacgctaa	aaacacaggc	2340
aattatgatg	aagtgaaaaa	agctcagaaa	gatcttgaaa	aatctctaag	gaaacgagag	2400
catttagaga	aagaagtaga	gaaaaaattg	gagagcaaaa	gcggcaacaa	aaataaaatg	2460
gaagcaaaag	ctcaagctaa	cagccaaaaa	gatgagattt	ttgcgttgat	caataaagag	2520
gctaatagag	acgcaagagc	aatcgcttac	gctcagaatc	ttaaaggcat	caaaagggaa	2580
ttgtctgata	aacttgaaaa	tgtcaacaag	aatttgaaag	actttgataa	atcttttgat	2640
gaattcaaaa	atggcaaaaa	taaggatttc	agcaaggcag	aagaaacact	aaaagccctt	2700
aaaggttcgg	tgaaagattt	aggtatcaat	ccagaatgga	tttcaaaagt	tgaaaacctt	2760
aatgcagctt	tgaatgaatt	caaaaatggc	aaaaataagg	atttcagcaa	ggtaacgcaa	2820
gcaaaaagcg	accttgaaaa	ttccgttaaa	gatgtgatca	tcaatcaaaa	ggtaacggat	2880
aaagttgata	atctcaatca	agcggtatca	gtggctaaag	caacgggtga	tttcagtagg	2940
gtagagcaag	cgtagccga	tctcaaaaat	ttctcaaagg	agcaattggc	ccaacaagct	3000
caaaaaaatg	aaagtctcaa	tgctagaaaa	aaatctgaaa	tatatcaatc	cgtaagaat	3060
ggtgtgaatg	gaaccctagt	cggtaatggg	ttatctcaag	cagaagccac	aactctttct	3120
aaaaactttt	cggacatcaa	gaaagagttg	aatgcaaaac	ttggaaattt	caataacaat	3180
aacaataatg	gactcaaaaa	cgaaccctatt	tatgctaaag	ttaataaaaa	gaaagcaggg	3240

caagcagcta	gccttgaaga	accattttac	gctcaagttg	ctaaaaaggt	aaatgcaaaa	3300
attgaccgac	tcaatcaa	agcaagtgg	ttgggtgttg	tagggcaagc	agcgggcttc	3360
cctttgaaaa	ggcatgataa	agttgatgat	ctcagtaagg	tagggctttc	aaggaaatcaa	3420
gaattggctc	agaaaattga	caatctcaat	caagcgggat	cagaagctaa	agcagggtttt	3480
tttggcaatc	tagagcaaac	gatagacaag	ctcaaagatt	ctacaaaaca	caatcccatg	3540
aatctatggg	ttgaaagtgc	aaaaaaagta	cctgctagtt	tgtcagcgaa	actagacaat	3600
tacgctacta	acagccacat	acgcattaat	agcaatatca	aaaatggagc	aatcaatgaa	3660
aaagcgaccg	gcatgctaac	gcaaaaaaac	cctgagtggc	tcaagctcgt	gaatgataag	3720
atagttgcgc	ataatgtagg	aagcgttcct	ttgtcagagt	atgataaaat	tggcttcaac	3780
cagaagaata	tgaagatta	ttctgattcg	ttcaagtttt	ccaccaagtt	gaacaatgct	3840
gtaaaagaca	ctaattcttg	ctttacgcaa	tttttaacca	atgcattttc	tacagcatct	3900
tattactgct	tggcgagaga	aaatgcggag	catggaatca	agaacgttaa	tacaaaaggt	3960
ggtttccaaa	aatcttaaag	gattaaggaa	tacaaaaaac	gcaaaaacca	ccccttgcta	4020
aaagcgaggg	gtttttta	actccttagc	agaaatccca	atcgtcttta	gtatttgggg	4080
tgaatgctac	caattcatgg	tatcatatcc	ccatacatte	gtatctagcg	taggaagtgt	4140
gcaaagttac	gcctttggag	atatgatgtg	tgagacctgt	aggggaatgcg	ttggagctca	4200
aactctgtaa	aatccctatt	atagggacac	agagtggaga	ccaaactctc	cctacgggca	4260
acatcagcct	aggaagccca	atcgtcttta	gcggttgggc	acttcacctt	aaaatatccc	4320
gacagacact	aacgaaaggc	tttgttcttt	aaagtctgca	tggatatttc	ctaccccaaa	4380
aagacttaac	cctttgctta	aaattaagtt	tgattgtgct	agtgggttcg	tgctatagtg	4440
cgaaaattaa	ttaagggtta	taaagagagc	ataaactaga	aaaaacaagt	agctataaca	4500
aagatcaagt	tcaaaaaatc	atagagcttt	tagagcaaat	tgatcgcgct	cttaacccaa	4560
gaaaaatcag	aaaaaccata	ggaattatca	cacctataa	tgcccaaaaa	agacgcttgc	4620
gatcagaagt	ggaaaaatac	ggcttcaaga	attttgatga	gctcaaaata	gacactgtgg	4680
atgcctttca	aggtgaagag	gcagatatta	ttattttatc	caccgtgaaa	acttgtggta	4740
atctttcttt	cttgctagat	tctaaacgct	tgaatgtggc	tatttctagg	gcaaaagaaa	4800
atctcatttt	tgtgggtaaa	aagtccttct	ttgagaattt	atgaagcgat	gagaagaata	4860
tcttttagcgc	tattttgcaa	gtctgtagat	aggtaatctt	ttccaaagat	aatcattaga	4920
cattcttcgc	ttcaaaacgc	tttcataaat	ctctctaaag	cgctttataa	tcaacacaat	4980
acccttatag	tgtgagctat	agcccctttt	tgggaattga	gttattttga	ctttaaattt	5040
ttattagcgt	tacaatttga	gccattcttt	agcttgtttt	tctagccaga	tcacatcgcc	5100
gctcgcatga	aattccactt	tagggaatgc	gtgtgcattt	tttttaaggg	cgtatttttg	5160
ctgcaaatat	cctacaatag	catcgccgga	atggatgagt	aggggggggtg	ttgaaagggc	5220
aaaatgctcc	ataaaatagc	cctcaatttt	ttgagcgatt	aagggaat	gcgtgcaacc	5280
taaaataatc	acttcgggaa	aatctttaag	ggagtgaat	aataacgcat	gcaagtttct	5340
aacaattcgc	cctctaaaat	actttcttca	atcaaaggca	caaaaagaga	agtggctaaa	5400
tgcgaaacat	tcaaatagcc	ttgttgtttc	agggcattgt	cataagcgtt	ggattggatc	5460
gtcgcttttg	tccctagcac	taaaataggg	gcggttttat	cttttacttg	tcgcttgatc	5520
gctaaaatgc	ttggctcaat	cacgcccaca	atagggattt	tggaatgctt	ttgcatctct	5580
tctaaagcta	gagcgctcgc	tgtgttgcat	gccacaatca	ataattcaat	ctggtgcggg	5640
ttgaaaaaat	ccaaagcctc	taagccaaat	tgcttgatcg	tagtgggggc	tttagtgcca	5700
taaggcactc	tagccgtatc	gccataatag	atgatttcat	caaataattg	cgcttttaaa	5760
aggcttttta	aaacgctaaa	ccctcccaca	ccgctatcaa	aaacgcctat	tttcatgaca	5820
ctttttta	ttaatgggat	taattagggg	ttttattttt	cattcattaa	gtttaaaaat	5880
tcttcattgt	ccttagtttg	ttgcatttta	gaatagacaa	agctt		5925

<210> 5

<211> 1147

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 5

Met	Thr	Asn	Glu	Thr	Ile	Asp	Gln	Gln	Pro	Gln	Thr	Glu	Ala	Ala	Phe
1				5					10					15	

Asn	Pro	Gln	Gln	Phe	Ile	Asn	Asn	Leu	Gln	Val	Ala	Phe	Leu	Lys	Val
		20						25					30		

Asp	Asn	Ala	Val	Ala	Ser	Tyr	Asp	Pro	Asp	Gln	Lys	Pro	Ile	Val	Asp
		35					40					45			

Lys	Asn	Asp	Arg	Asp	Asn	Arg	Gln	Ala	Phe	Glu	Gly	Ile	Ser	Gln	Leu
	50					55				60					

Arg	Glu	Glu	Tyr	Ser	Asn	Lys	Ala	Ile	Lys	Asn	Pro	Thr	Lys	Lys	Asn
65					70					75					80

Gln	Tyr	Phe	Ser	Asp	Phe	Ile	Asn	Lys	Ser	Asn	Asp	Leu	Ile	Asn	Lys
				85					90					95	

Asp	Asn	Leu	Ile	Asp	Val	Glu	Ser	Ser	Thr	Lys	Ser	Phe	Gln	Lys	Phe
		100						105					110		

Gly	Asp	Gln	Arg	Tyr	Arg	Ile	Phe	Thr	Ser	Trp	Val	Ser	His	Gln	Asn
	115						120					125			

Asp	Pro	Ser	Lys	Ile	Asn	Thr	Arg	Ser	Ile	Arg	Asn	Phe	Met	Glu	Asn
	130					135					140				

Ile	Ile	Gln	Pro	Pro	Ile	Leu	Asp	Asp	Lys	Glu	Lys	Ala	Glu	Phe	Leu
145					150					155					160

Lys	Ser	Ala	Lys	Gln	Ser	Phe	Ala	Gly	Ile	Ile	Ile	Gly	Asn	Gln	Ile
			165						170					175	

Arg	Thr	Asp	Gln	Lys	Phe	Met	Gly	Val	Phe	Asp	Glu	Ser	Leu	Lys	Glu
		180						185						190	

Arg	Gln	Glu	Ala	Glu	Lys	Asn	Gly	Glu	Pro	Thr	Gly	Gly	Asp	Trp	Leu
	195						200					205			

Asp	Ile	Phe	Leu	Ser	Phe	Ile	Phe	Asp	Lys	Lys	Gln	Ser	Ser	Asp	Val	210	215	220	
Lys	Glu	Ala	Ile	Asn	Gln	Glu	Pro	Val	Pro	His	Val	Gln	Pro	Asp	Ile	225	230	235	240
Ala	Thr	Thr	Thr	Thr	Asp	Ile	Gln	Gly	Leu	Pro	Pro	Glu	Ala	Arg	Asp	245	250	255	
Leu	Leu	Asp	Glu	Arg	Gly	Asn	Phe	Ser	Lys	Phe	Thr	Leu	Gly	Asp	Met	260	265	270	
Glu	Met	Leu	Asp	Val	Glu	Gly	Val	Ala	Asp	Ile	Asp	Pro	Asn	Tyr	Lys	275	280	285	
Phe	Asn	Gln	Leu	Leu	Ile	His	Asn	Asn	Ala	Leu	Ser	Ser	Val	Leu	Met	290	295	300	
Gly	Ser	His	Asn	Gly	Ile	Glu	Pro	Glu	Lys	Val	Ser	Leu	Leu	Tyr	Gly	305	310	315	320
Gly	Asn	Gly	Gly	Pro	Gly	Ala	Arg	His	Asp	Trp	Asn	Ala	Thr	Val	Gly	325	330	335	
Tyr	Lys	Asp	Gln	Gln	Gly	Asn	Asn	Val	Ala	Thr	Ile	Ile	Asn	Val	His	340	345	350	
Met	Lys	Asn	Gly	Ser	Gly	Leu	Val	Ile	Ala	Gly	Gly	Glu	Lys	Gly	Ile	355	360	365	
Asn	Asn	Pro	Ser	Phe	Tyr	Leu	Tyr	Lys	Glu	Asp	Gln	Leu	Thr	Gly	Ser	370	375	380	
Gln	Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Ile	Asp	Phe	Met	385	390	395	400
Glu	Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Glu	Lys	405	410	415	
Glu	Lys	Glu	Lys	Phe	Arg	Thr	Glu	Ile	Lys	Asp	Phe	Gln	Lys	Asp	Ser	420	425	430	
Lys	Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	Arg	Ile	Ala	Phe	Val	Ser	435	440	445	
Lys	Lys	Asp	Thr	Lys	His	Ser	Ala	Leu	Ile	Thr	Glu	Phe	Gly	Asn	Gly	450	455	460	

Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	465	470	475	480
Leu	Asp	Arg	Glu	Lys	Asn	Val	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	485	490	495	
Gly	Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	500	505	510	
Lys	Asn	Pro	Asn	Lys	Gly	Val	Gly	Val	Thr	Asn	Gly	Val	Ser	His	Leu	515	520	525	
Glu	Val	Gly	Phe	Asn	Lys	Val	Ala	Ile	Phe	Asn	Leu	Pro	Asp	Leu	Asn	530	535	540	
Asn	Leu	Ala	Ile	Thr	Ser	Phe	Val	Arg	Arg	Asn	Leu	Glu	Asp	Lys	Leu	545	550	555	560
Thr	Thr	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Ile	Lys	Asp	565	570	575	
Phe	Leu	Ser	Ser	Asn	Lys	Glu	Leu	Val	Gly	Lys	Thr	Leu	Asn	Phe	Asn	580	585	590	
Lys	Ala	Val	Ala	Asp	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	595	600	605	
Lys	Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Arg	Lys	Arg	Glu	His	Leu	610	615	620	
Glu	Lys	Glu	Val	Glu	Lys	Lys	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	625	630	635	640
Lys	Met	Glu	Ala	Lys	Ala	Gln	Ala	Asn	Ser	Gln	Lys	Asp	Glu	Ile	Phe	645	650	655	
Ala	Leu	Ile	Asn	Lys	Glu	Ala	Asn	Arg	Asp	Ala	Arg	Ala	Ile	Ala	Tyr	660	665	670	
Ala	Gln	Asn	Leu	Lys	Gly	Ile	Lys	Arg	Glu	Leu	Ser	Asp	Lys	Leu	Glu	675	680	685	
Asn	Val	Asn	Lys	Asn	Leu	Lys	Asp	Phe	Asp	Lys	Ser	Phe	Asp	Glu	Phe	690	695	700	
Lys	Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	705	710	715	720

Ala	Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile			
				725					730					735				
Ser	Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly			
			740					745					750					
Lys	Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu			
		755					760					765						
Asn	Ser	Val	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Val	Thr	Asp	Lys	Val			
	770					775						780						
Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe			
785					790					795					800			
Ser	Arg	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu			
				805					810					815				
Gln	Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Arg	Lys			
			820					825					830					
Lys	Ser	Glu	Ile	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu			
		835					840					845						
Val	Gly	Asn	Gly	Leu	Ser	Gln	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn			
	850					855					860							
Phe	Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn			
865					870					875					880			
Asn	Asn	Asn	Asn	Asn	Gly	Leu	Lys	Asn	Glu	Pro	Ile	Tyr	Ala	Lys	Val			
				885					890					895				
Asn	Lys	Lys	Lys	Ala	Gly	Gln	Ala	Ala	Ser	Leu	Glu	Glu	Pro	Ile	Tyr			
			900					905						910				
Ala	Gln	Val	Ala	Lys	Lys	Val	Asn	Ala	Lys	Ile	Asp	Arg	Leu	Asn	Gln			
			915					920				925						
Ile	Ala	Ser	Gly	Leu	Gly	Val	Val	Gly	Gln	Ala	Ala	Gly	Phe	Pro	Leu			
	930						935					940						
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg			
945					950					955					960			
Asn	Gln	Glu	Leu	Ala	Gln	Lys	Ile	Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser			
				965					970					975				

Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys
980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser
995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
1010 1015 1020

Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly Ala Ile
1025 1030 1035 1040

Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu
1045 1050 1055

Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro
1060 1065 1070

Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
1075 1080 1085

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val Lys
1090 1095 1100

Asp Thr Asn Ser Gly Phe Thr Gln Phe Leu Thr Asn Ala Phe Ser Thr
1105 1110 1115 1120

Ala Ser Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly Ile Lys
1125 1130 1135

Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser
1140 1145

<210> 6
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
Sequence

<400> 6
Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro

20	25	30
Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile		
35	40	45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro		
50	55	60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr		
65	70	75
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr		
85	90	95
Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro		
100	105	110
Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn		
115	120	125
Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr		
130	135	140
Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu		
145	150	155
Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val		
165	170	175
Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met		
180	185	190
Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu		
195	200	205
Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys		
210	215	220
Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met		
225	230	235
Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu		
245	250	255
Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile		
260	265	270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu		

275		280		285
Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu				
290		295		300
Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly				
305		310		315
Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly				
	325		330	335
His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile				
	340		345	350
Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu				
	355		360	365
Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser				
	370		375	380
Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser				
385		390		395
Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala				
	405		410	415
Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp				
	420		425	430
Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu				
	435		440	445
Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn				
	450		455	460
Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly				
465		470		475
Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val				
	485		490	495
Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu				
	500		505	510
Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro				
	515		520	525
Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly				

530

535

540

Met Met

545

<210> 7

<211> 1838

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 7

```

aagcttgctg tcatgatcac aaaaaacact aaaaaacatt attattaagg atacaaaatg 60
gcaaaagaaa tcaaattttc agatagtgcg agaaaccttt tatttgaagg cgtgaggcaa 120
ctccatgacg ctgtcaaagt aaccatgggg ccaagaggca ggaatgtatt gatccaaaaa 180
agctatggcg ctccaagcat caccaaagac ggcgtgagcg tggctaaaga gattgaatta 240
agttgcccg tagctaacat gggcgctcaa ctcgttaaag aagtagcgag caaaaccgct 300
gatgctgccg gcgatggcac gaccacagcg accgtgctag cttatagcat ttttaaagaa 360
ggtttgagga atatcacggc tggggctaac cctattgaag tgaaacgagg catggataaa 420
gctgctgaag cgatcattaa tgagcttaaa aaagcgagca aaaaagtagg cggtaaagaa 480
gaaatcacc aagtggcgac cattttctgca aactcgcgc acaatatcg gaaactcatc 540
gctgacgcta tggaaaaagt gggtaaagac ggcgtgatca ccgttgagga agctaagggc 600
attgaagatg aattggatgt cgtagaaggc atgcaatttg atagaggcta cctctccct 660
tattttgtaa cgaacgctga gaaaatgacc gctcaattgg ataatgctta catcctttta 720
acggataaaa aaatctctag catgaaagac attctccgc tactagaaaa aaccatgaaa 780
gagggcaaac cgcttttaat catcgctgaa gacattgagg gcgaagcttt aacgactcta 840
gtggtgaata aattaagagg cgtgttgaat atcgagcgg ttaaagctcc aggctttggg 900
gacagaagaa aagaaatgct caaagacatc gctattttta ccggcgggtca agtcattagc 960
gaagaattgg gcttgagtct agaaaacgct gaagtggagt ttttaggcaa agctggaagg 1020
attgtgattg acaaagacaa caccacgac gtatagtgga aaggccatag cgatgatgtt 1080
aaagacagag tcgcgagat caaaaccaa attgcaagta cgacaagcga ttatgacaaa 1140
gaaaaattgc aagaaagatt ggctaaactc tctggcggtg tggctgtgat taaagtgggc 1200
gctgagagtg aagtggaaat gaaagagaaa aaagaccggg tggatgacgc gttgagcgcg 1260
actaaagcgg cggttgaaga aggcattgtg attggtggcg gtgcggctct cattcgcgcg 1320
gctcaaaaag tgcatttgaa tttgcacgat gatgaaaaag tgggctatga aatcatcatg 1380
cgcgccatta aagccccatt agctcaaata gctatcaacg ctggttatga tggcgggtgtg 1440
gtcgtgaatg aagtagaaaa acacgaaggg cattttggtt ttaacgctag caatggcaag 1500
tatgtggata tgtttaaaga aggcattatt gacccttaa aagtagaaag gatcgctcta 1560
caaaatgcgg tttcggtttc aagcctgctt ttaaccacag aagccaccgt gcatgaaatc 1620
aaagaagaaa aagcgactcc ggcaatgcct gatatgggtg gcatgggcgg tatgggaggc 1680
atgggcggca tgatgtaagc ccgcttgctt tttagtataa tctgctttta aaatcccttc 1740
tctaaatccc cccctttcta aaatctcttt tttggggggg tgctttgata aaaccgctcg 1800
cttgtaaaaa catgcaacaa aaaatctctg ttaagctt 1838

```

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 8

gactcgagtc gacatcga

18

6
ant